

CLAIMS:

1-33 (Canceled)

34. (Previously Presented) A nucleic acid molecule encoding a fusion protein comprising aa) the first N-terminal domain of the gene III protein of filamentous phage and ab) a (poly)peptide which is encoded by a nucleic acid sequence comprised in a genomic DNA fragment or an expressed sequence tag (EST) from a eukaryotic cell, wherein said nucleic acid molecule does not comprise a nucleic acid sequence encoding a signal sequence for the transport of the fusion protein to the periplasm of a bacterial host cell, and wherein said genomic DNA fragment or expressed sequence tag (EST) is between 100 and 2000 base pairs in length and is derived from a eukaryotic organism.

35. (Previously presented) A vector comprising a nucleic acid molecule according to claim 34.

36. (Previously presented) The vector according to claim 35 which is an expression vector.

37. (Previously presented) A host cell comprising a nucleic acid according to claim 34.

38. (Previously presented) The host cell according to claim 37 which is an E.coli cell.

39. (Canceled)

40. (Previously presented) A method for the expression of a (poly)peptide/protein comprising:

expressing a nucleic acid molecule encoding a fusion protein in a host cell under conditions that allow the formation of inclusion bodies comprising said fusion protein, wherein said nucleic acid molecule comprises a genomic DNA fragment or EST sequence derived from a eukaryotic organism that is 100 to 2000 base pairs long linked to a nucleic acid sequence that encodes the first N-terminal domain of the geneIII protein of filamentous phage.

41. (Previously presented) The method of claim 40 further comprising the steps of
b) isolating said inclusion bodies; and

c) solubilising said fusion protein under suitable conditions.

42. (Previously presented) A host cell comprising a vector according to claim 35.

43. (Previously presented) A host cell comprising a vector according to claim 36.

44. (New) The method of claim 34, wherein the genomic DNA fragment or EST sequence derived from a eukaryotic organism is 200 to 1500 base pairs long.

45. (New) The method of claim 40, wherein the genomic DNA fragment or EST sequence derived from a eukaryotic organism is 200 to 1500 base pairs long.